

SEQUENCE LISTING

<110> Bates, Elizabeth
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Garrone, Pierre

<120> MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

<130> SF0977X

<140> 09/869,388

<141> 1999-12-29

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<212> DNA

<213> homo sapiens

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ctcacctcaa cccccaggcg gccctccac agggccctc tcttgccctgg acggctctgc 120

tggtctcccc gtccccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174
Met Gly Arg Pro Leu Leu Leu
-19 -15

ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222
Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly
-10 -5 1

tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270
Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys
5 10 15 20

cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc 318
His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe
25 30 35

tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp 40 45 50	366
aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro 55 60 65	414
tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu 70 75 80	462
ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp 85 90 95 100	510
cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly 105 110 115	558
agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln 120 125 130	606
gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp 135 140 145	654
agg ctc agt agc aca acc acc aca acc ggc ctc agg gtc aca cag ggc Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly 150 155 160	702
aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly 165 170 175 180	750
gtg gca gtg gct gtc act gtg ctc gga atc atg att ttg gga ctg atc Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile 185 190 195	798
tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala 200 205 210	846
aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu 215 220 225	894
aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys 230 235 240	942
gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser 245 250 255 260	990

ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag 1038
 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
 265 270 275

acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa 1092
 Thr Leu Tyr Ser Val Leu Lys Ala
 280

tggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa gcctgaggca 1152

gaatcaagtg agcccaggag ttcagggcca gctttgataa tggagcgaga tgccatctct 1212

agttaaaaat atatattaac aataaagtaa caaatatt 1249

<210> 2
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 <212> PRT
 <213> homo sapiens

<400> 2
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 -19 -15 -10 -5

Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
 1 5 10

Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
 15 20 25

Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
 30 35 40 45

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
 80 85 90

Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 95 100 105

Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
 110 115 120 125

Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
 130 135 140

Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr
 145 150 155

Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
 160 165 170

Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
 175 180 185

Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
 190 195 200 205

Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
 210 215 220

Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
 225 230 235

Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
 240 245 250

Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
 255 260 265

Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
 270 275 280

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 <222> (130)..(180)

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ctccacaggg cccctctcct gcctggacgg ctctgctggt ctccccgtcc cctggagaag 120

aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg 168
 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu
 -17 -15 -10 -5

ctg ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca 216
 Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro
 1 5 10

agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg 264
 Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met
 15 20 25

ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu 30 35 40	312
gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His 45 50 55 60	360
ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr 65 70 75	408
gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe 80 85 90	456
ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys 95 100 105	504
cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser 110 115 120	552
atc gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys 125 130 135 140	600
gcc aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr 145 150 155	648
gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro 160 165 170	696
aag gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr 175 180 185	744
tca ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn 190 195 200	792
gag acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct Glu Thr Leu Tyr Ser Val Leu Lys Ala 205 210	839
caagactgaa tgggtgaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa	899
gcctgaggca gaatcaagtg agcccaggag ttcagggcca gctt	943

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<400> 4

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-17 -15 -10 -5

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1 5 10 15

Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
20 25 30

Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
35 40 45

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
50 55 60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
65 70 75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
80 85 90 95

Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
100 105 110

Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
115 120 125

Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr
130 135 140

Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile
145 150 155

Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp
160 165 170 175

Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg
180 185 190

Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu Thr Leu
195 200 205

Tyr Ser Val Leu Lys Ala
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<211> 1450

<212> DNA

<213> homo sapiens

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<222> (386)..(436)

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cagaagccag gcatagcgcg ctggctagga ctccagtacc gtgaagggag gcagtgaagag 120
cagacatctg tgcctcattc ctgatctcaa ggggaaagca agaacaaggg aggcttcctc 180
aggatctcga acctgcggaa ggaggaccag tctgtgtact tctgccaagt ccagctggac 240
atacagatca gggaggctgt cgtggcagtc catcaagggg acccacctca ccatcaccca 300
ggccctcagg cagccctcc acaggggccc tctcctgcct ggacagctct gctgggtctcc 360
ccgtcccctg gagaagaaca aggcc atg ggt cgg ccc ctg ctg ctg ccc ctg 412
Met Gly Arg Pro Leu Leu Leu Pro Leu
-17 -15 -10
ctg ctc ctg ctg cag ccg cca gca ttt ctg cag cct ggt ggc tcc aca 460
Leu Leu Leu Leu Gln Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr
-5 1 5
gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa cac ctc 508
Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu
10 15 20
tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac 556
Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr
25 30 35 40
ccc tgg gag tta gcc ata gtt ccc aac gtg aga ata tcc tgg aga cgg 604
Pro Trp Glu Leu Ala Ile Val Pro Asn Val Arg Ile Ser Trp Arg Arg
45 50 55
ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct tcc att 652
Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile
60 65 70
cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag 700
His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln
75 80 85
gag agc ggc ttc ctc agg atc tca aac ctg cgg aag gag gac cag tct 748
Glu Ser Gly Phe Leu Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser
90 95 100
gtg tat ttc tgc cga gtc gag ctg gac acc cgg aga tca ggg agg cag 796
Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln
105 110 115 120

cag ttg cag tcc atc aag ggg acc aaa ctc acc atc acc cag gct gtc Gln Leu Gln Ser Ile Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val 125 130 135	844
aca acc acc acc acc tgg agg ccc agc agc aca acc acc ata gcc ggc Thr Thr Thr Thr Thr Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly 140 145 150	892
ctc agg gtc aca gaa agc aaa ggg cac tca gaa tca tgg cac cta agt Leu Arg Val Thr Glu Ser Lys Gly His Ser Glu Ser Trp His Leu Ser 155 160 165	940
ctg gac act gcc atc agg gtt gca ttg gct gtc gct gtg ctc aaa act Leu Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr 170 175 180	988
gtc att ttg gga ctg ctg tgc ctc ctc ctc ctg tgg tgg agg aga agg Val Ile Leu Gly Leu Leu Cys Leu Leu Leu Leu Trp Trp Arg Arg Arg 185 190 195 200	1036
aaa ggt agc agg gcg cca agc agt gac ttc tgaccaacag agtgtgggga Lys Gly Ser Arg Ala Pro Ser Ser Asp Phe 205 210	1086
gaagggatgt gtattagccc cggaggacgt gatgtgagac ccgcttgtga gtcctccaca	1146
ctcgttcccc attggcaaga tacatggaga gcaccctgag gacctttaaa aggcaaagcc	1206
gcaaggcaga aggaggctgg gtccctgaat caccgactgg aggagagtta cctacaagag	1266
ccttcatcca ggagcatcca cactgcaatg atataggaat gaggtctgaa ctccactgaa	1326
ttaaaccact ggcatttggg ggctgtttat tatagcagtg caaagagttc ctttatectc	1386
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aaaa	1450

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 <212> PRT
 <213> homo sapiens

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 1 5 10 15
 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
 20 25 30
 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val
 35 40 45

Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
 50 55 60
 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
 65 70 75
 Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
 80 85 90 95
 Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
 100 105 110
 Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
 115 120 125
 Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg
 130 135 140
 Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
 145 150 155
 Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
 160 165 170 175
 Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
 180 185 190
 Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser
 195 200 205
 Ser Asp Phe
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 <212> DNA
 <213> homo sapiens

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 <222> (130)..(180)

<220>
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 <222> (181)..(654)

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 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg ctg 171

Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu
 -15 -10 -5

ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca agc 219
 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser
 -1 1 5 10

tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg ggt 267
 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25

ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 315
 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45

aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60

cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 411
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75

aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
 80 85 90

agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga 507
 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105

gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555
 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
 110 115 120 125

gag ggg acc aaa ctc tcc atc acc cag ggg aac cct tcc aaa aca cag 603
 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
 130 135 140

agg agc cat atg aga ata tca gga atg aag gac aaa ata cag atc cca 651
 Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
 145 150 155

agc taa atcccaagga tgacggcatc gtctatgctt cccttgccct ctccagctcc 707
 Ser

acctcaccca gagcacctcc cagccaccgt cccctcaaga gccccagaa cgagaccctg 767

tactctgtct taaaggccta accaatggac agccctctca agactgaatg gtgaggccag 827

gtacagtggc gcacacctgt aatcccagct actctgaagc ctgaggcaga atcaagtgag 887

cccaggagtt cagggccagc tt 909

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 <211> 175

<212> PRT
<213> homo sapiens

<400> 8

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-1 1 5 10

Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
15 20 25

Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
30 35 40 45

Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
50 55 60

Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
65 70 75

Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu
80 85 90

Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg
95 100 105

Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile
110 115 120 125

Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Asn Pro Ser Lys Thr Gln
130 135 140

Arg Ser His Met Arg Ile Ser Gly Met Lys Asp Lys Ile Gln Ile Pro
145 150 155

Ser

<210> 9

<211> 1459

<212> DNA

<213> homo sapiens

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<221> CDS

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<222> (309)..(359)

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<221> mat_peptide

<222> (360)..(986)

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 ataaaggaag tgctggtcac cctggaggtg tactggtttg gggaagggtcc ccggccccca 180
 cagccctctg gggagcctca ccctggctct cccactcac ctcagccctc aggcagcccc 240
 tccacaggac ccctctctg cctggacagc tctgctggtc tccccgtccc ctggagaaga 300
 acaaggcc atg ggt cgg ccc ctg ctg ctg ccc ctg ctg ctc ctg ctg cag 350
 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu Gln
 -15 -10 -5
 ccg cca gca ttt ctg cag cct ggt ggc tcc aca gga tct ggt cca agc 398
 Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser
 -1 1 5 10
 tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg ggt 446
 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
 15 20 25
 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 494
 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
 30 35 40 45
 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 542
 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
 50 55 60
 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 590
 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val
 65 70 75
 aac cgg ctc ttt ctg aac tgg aca gag ggt cag gag agc ggc ttc ctc 638
 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
 80 85 90
 agg atc tca aac ctg cgg aag gag gac cag tct gtg tat ttc tgc cga 686
 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
 95 100 105
 gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc 734
 Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
 110 115 120 125
 aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc 782
 Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr
 130 135 140
 tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa 830
 Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu
 145 150 155
 agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc 878
 Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
 160 165 170

agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg 926
 Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu
 175 180 185

ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca 974
 Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro
 190 195 200 205

agc agt gac ttc tga ccaacagagt gtggggagaa gggatgtgta ttagccccgg 1029
 Ser Ser Asp Phe

aggacgtgat gtgagacccg cttgtgagtc ctccacactc gttccccatt ggcaagatac 1089
 atggagagca ccctgaggac ctttaaaagg caaagccgca aggcagaagg aggctgggtc 1149
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 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
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Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
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Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
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Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr
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Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
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